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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,372E

DATE: 04/02/2003

TIME: 12:41:45

Input Set : A:\61302 Seq Listing.txt
 Output Set: N:\CRF4\04022003\J017372E.raw

3 <110> APPLICANT: Wolfraim, Lawrence A
 4 Letterio, John J
 6 <120> TITLE OF INVENTION: FUNCTIONALIZED TGF-BETA FUSION PROTEINS
 8 <130> FILE REFERENCE: 4239-61302
 10 <140> CURRENT APPLICATION NUMBER: US 10/017,372E
 11 <141> CURRENT FILING DATE: 2001-10-19
 13 <150> PRIOR APPLICATION NUMBER: US 60/242,292
 14 <151> PRIOR FILING DATE: 2000-10-20
 16 <160> NUMBER OF SEQ ID NOS: 39
 18 <170> SOFTWARE: PatentIn version 3.2
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 28
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Artificial Sequence
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Primer
 28 <400> SEQUENCE: 1
 29 ggagagatct ggtaccgaga tggcgctt 28
 32 <210> SEQ ID NO: 2
 33 <211> LENGTH: 42
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Artificial Sequence
 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: Primer
 40 <400> SEQUENCE: 2
 41 ataagaattt cggccgcattt aatcgatccc aagtgggctt gg 42
 44 <210> SEQ ID NO: 3
 45 <211> LENGTH: 48
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Artificial Sequence
 49 <220> FEATURE:
 50 <223> OTHER INFORMATION: Primer
 52 <400> SEQUENCE: 3
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 56 <210> SEQ ID NO: 4
 57 <211> LENGTH: 45
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Primer
 64 <400> SEQUENCE: 4
 65 ctgtcgatcg tcatccttgt agtctcgccg gtgcgggag ctgtg 45
 68 <210> SEQ ID NO: 5

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69 <211> LENGTH: 45
70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Primer
76 <400> SEQUENCE: 5
77 gactacaagg atgacgacga caggagaaga actgctgcgt gcggc 45
80 <210> SEQ ID NO: 6
81 <211> LENGTH: 45
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: Primer
88 <400> SEQUENCE: 6
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92 <210> SEQ ID NO: 7
93 <211> LENGTH: 8
94 <212> TYPE: PRT
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Synthetic oligopeptide
100 <400> SEQUENCE: 7
102 Asp Tyr Lys Asp Asp Asp Asp Lys
103 1 5
106 <210> SEQ ID NO: 8
107 <211> LENGTH: 1197
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion
Construct
115 <220> FEATURE:
116 <221> NAME/KEY: CDS
117 <222> LOCATION: (1)..(1197)
118 <223> OTHER INFORMATION: Protein coding sequence
120 <220> FEATURE:
121 <221> NAME/KEY: misc_feature
122 <222> LOCATION: (278)..(279)
123 <223> OTHER INFORMATION: Maturation cleavage site (relates to amino acid residue
nos.)
125 <400> SEQUENCE: 8
126 atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ccg ctg ctg 48
127 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
128 1 5 10 15
130 tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gca ctg tcc acc 96
131 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
132 20 25 30
134 tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 144
135 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
136 35 40 45
138 att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccc agc 192

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139	Ile	Arg	Gly	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Ala	Ser	Pro	Pro	Ser	
140	50				55				60								
142	cag	ggg	gac	gtg	ccg	ccc	ggc	ccg	ctg	cct	gag	gca	gta	ctg	gct	ctt	240
143	Gln	Gly	Asp	Val	Pro	Pro	Gly	Pro	Leu	Pro	Glu	Ala	Val	Leu	Ala	Leu	
144	65				70				75			80					
146	tac	aac	agt	acc	cgc	gac	cg	gt	gcc	ggg	gaa	agt	gtc	gaa	ccg	gag	288
147	Tyr	Asn	Ser	Thr	Arg	Asp	Arg	Val	Ala	Gly	Glu	Ser	Val	Glu	Pro	Glu	
148						85			90			95					
150	ccc	gag	cca	gag	g	gg	g	g	ac	cc	g	cc	gt	ct	ct	336	
151	Pro	Glu	Pro	Glu	Ala	Asp	Tyr	Tyr	Ala	Lys	Glu	Val	Thr	Arg	Val	Leu	
152					100				105			110					
154	atg	gt	gaa	agc	ggc	aa	atc	at	gat	aa	ttc	aag	ggc	acc	ccc	384	
155	Met	Val	Glu	Ser	Gly	Asn	Gln	Ile	Tyr	Asp	Lys	Phe	Lys	Gly	Thr	Pro	
156						115			120			125					
158	cac	agc	tta	tat	atg	ctg	ttc	aa	ac	ac	tcg	gag	ctc	cg	g	gt	432
159	His	Ser	Leu	Tyr	Met	Leu	Phe	Asn	Thr	Ser	Glu	Leu	Arg	Glu	Ala	Val	
160						130			135			140					
162	ccg	gaa	cct	gta	ttg	ctc	tct	cg	gca	gag	ctg	cg	ctg	ctg	agg	ctc	480
163	Pro	Glu	Pro	Val	Leu	Leu	Ser	Arg	Ala	Glu	Leu	Arg	Leu	Leu	Arg	Leu	
164	145					150				155			160				
166	aag	tta	aaa	gt	gag	ca	g	ca	gt	gag	ct	ta	ca	g	aa	ta	452
167	Lys	Leu	Lys	Val	Glu	Gln	His	Val	Glu	Leu	Tyr	Gln	Lys	Tyr	Ser	Asn	
168						165			170			175					
170	gat	tcc	tgg	cg	tc	tc	ag	ac	cg	ct	ct	gg	cc	ag	gt	ca	576
171	Asp	Ser	Trp	Arg	Tyr	Leu	Ser	Asn	Arg	Leu	Leu	Ala	Pro	Ser	Asp	Ser	
172						180			185			190					
174	ccg	gag	tgg	ctg	tcc	ttt	gat	gt	ac	gg	gtt	gt	cg	ca	tg	ct	624
175	Pro	Glu	Trp	Leu	Ser	Phe	Asp	Val	Thr	Gly	Val	Val	Arg	Gln	Trp	Leu	
176						195			200			205					
178	acc	cg	ca	g	ag	g	ct	at	g	gt	ttt	cg	ca	tg	ct	672	
179	Thr	Arg	Arg	Glu	Ala	Ile	Glu	Gly	Phe	Arg	Leu	Ser	Ala	His	Ser	Ser	
180						210			215			220					
182	tct	gac	agc	aaa	gat	aa	ca	ct	ca	gt	gaa	ttt	aa	cc	gg	tt	720
183	Ser	Asp	Ser	Lys	Asp	Asn	Thr	Leu	His	Val	Glu	Ile	Asn	Gly	Phe	Asn	
184	225					230				235			240				
186	tct	gg	cg	cg	gg	gt	gac	ct	gg	ac	ttt	ca	gg	at	gg	cc	768
187	Ser	Gly	Arg	Arg	Gly	Asp	Leu	Ala	Thr	Ile	His	Gly	Met	Asn	Arg	Pro	
188						245				250			255				
190	ttc	ct	ct	at	g	cc	ac	cc	ct	gg	ag	gg	cc	ca	ct	ca	816
191	Phe	Leu	Leu	Leu	Met	Ala	Thr	Pro	Leu	Glu	Arg	Ala	Gln	His	Leu	His	
192						260			265			270					
194	agc	tcc	cg	ca	cg	ca	g	ac	ta	aa	g	at	g	ac	aa	gg	648
195	Ser	Ser	Arg	His	Arg	Arg	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Ala	Leu	
196						275			280			285					
198	gat	acc	aa	ac	ta	tgc	ttc	ac	ac	gg	aa	ac	tgc	tgc	gt	cg	912
199	Asp	Thr	Asn	Tyr	Cys	Phe	Ser	Ser	Thr	Glu	Lys	Asn	Cys	Cys	Val	Arg	
200						290			295			300					
202	cag	ctc	ta	tt	gac	ttc	cg	aa	gac	ct	gg	aa	tg	tt	tt	at	960
203	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	Asp	Leu	Gly	Trp	Lys	Trp	Ile	His	

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204	305	310	315	320	
206	gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac				1008
207	Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr				
208	325	330	335		
210	atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac				1056
211	Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn				
212	340	345	350		
214	cag cac aac ccg ggc gcg tcg gcg ccg tgc tgc gtg ccg cag gcg				1104
215	Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala				
216	355	360	365		
218	ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg				1152
219	Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val				
220	370	375	380		
222	gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga				1197
223	Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser				
224	385	390	395		
227	<210> SEQ ID NO: 9				
228	<211> LENGTH: 398				
229	<212> TYPE: PRT				
230	<213> ORGANISM: Artificial Sequence				
232	<220> FEATURE:				
233	<223> OTHER INFORMATION: Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion Construct				

235	<400> SEQUENCE: 9				
237	Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu				
238	1	5	10	15	
241	Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr				
242	20	25	30		
245	Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala				
246	35	40	45		
249	Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser				
250	50	55	60		
253	Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu				
254	65	70	75	80	
257	Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu				
258	85	90	95		
261	Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu				
262	100	105	110		
265	Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro				
266	115	120	125		
269	His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val				
270	130	135	140		
273	Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu				
274	145	150	155	160	
277	Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn				
278	165	170	175		
281	Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser				
282	180	185	190		
285	Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu				
286	195	200	205		

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289 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
 290 210 215 220
 293 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
 294 225 230 235 240
 297 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
 298 245 250 255
 301 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
 302 260 265 270
 305 Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Lys Ala Leu
 306 275 280 285
 309 Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
 310 290 295 300
 313 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
 314 305 310 315 320
 317 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
 318 325 330 335
 321 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
 322 340 345 350
 325 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
 326 355 360 365
 329 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
 330 370 375 380
 333 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
 334 385 390 395
 337 <210> SEQ ID NO: 10
 338 <211> LENGTH: 363
 339 <212> TYPE: DNA
 340 <213> ORGANISM: Artificial Sequence
 342 <220> FEATURE:
 343 <223> OTHER INFORMATION: Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion
 Construct
 345 <400> SEQUENCE: 10
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 348 aagaactgct gcgtgcggca gctctacatt gacttccgga aggacctggg ctggaagtgg 120
 350 attcatgaac ccaagggtca ccatgccaat ttctgcctgg ggccctgtcc ctacatctgg 180
 352 agcctagaca ctcagtacag caaggtcctg gctctgtaca accagcacaa cccgggcgcg 240
 354 tcggcggcgc cgtgctgcgt gccgcaggcg ctggagccac tgccccatcgt gtactacgtg 300
 356 ggccgcaagc ccaaggtgga gcagctgtcc aacatgatcg tgcgttccctg caagtgcagc 360
 358 tga 363
 361 <210> SEQ ID NO: 11
 362 <211> LENGTH: 120
 363 <212> TYPE: PRT
 364 <213> ORGANISM: Artificial Sequence
 366 <220> FEATURE:
 367 <223> OTHER INFORMATION: Porcine (Sus scrofa) TGF-beta1/N-terminal FLAG Fusion
 Construct
 370 <220> FEATURE:
 371 <221> NAME/KEY: PEPTIDE
 372 <222> LOCATION: (1)..(8)
 373 <223> OTHER INFORMATION: FLAG tag
 375 <400> SEQUENCE: 11

VERIFICATION SUMMARY

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